In the Claims:

Please amend claims 1 and 2 as set forth below in the Listing of Claims:

Claim 1 (Currently Amended): A method of detecting a predisposition to allergic bronchopulmonary aspergillosis, said method comprising steps of:

(1) designing and synthesizing oligonucleotide primers capable of amplifying Exon 4 of human SP-A2 gene,

(2) amplifying genomic DNA of allergic bronchopulmonary aspergillosis patients and normal control individuals using said primers of step (~~a~~ 1),

(3) sequencing the amplified genomic DNA and identify sequence variations of the amplified genomic DNA computationally by comparing it with an existing sequence of human SP-A2 gene,

(4) screening normal control individuals and allergic bronchopulmonary aspergillosis patients for single nucleotide polymorphisms by sequencing of the amplified genomic DNA of the individuals using the said primers of step (~~a~~ 1),

(5) computing the frequency of G/C haplotypes at 1649 position and A/G haplotypes at 1660 position of allergic bronchopulmonary aspergillosis patients and normal control individuals,

(6) establishing the association of G (at 1649 position) and G (at 1660 position) haplotypes with the allergic bronchopulmonary aspergillosis disease based on their frequency distribution in normal individuals and allergic bronchopulmonary aspergillosis patients, and

(7) predicting the risk or susceptibility to allergic bronchopulmonary aspergillosis based on the haplotype present at the polymorphic sites in the individual tested, C (at 1649 position) and A (at 1660 position) haplotypes being at low risk and G (at 1649 position) and G (at 1660 position) haplotypes at high risk to the allergic bronchopulmonary aspergillosis.

Claim 2 (Currently Amended): A method as claimed in claim 1 wherein the oligonucelotide primers capable for amplification of said Exon 4 of said SP-A2 gene are selected from the group consisting of:

(a) 5' TGC CTG GAG CCC CTG GTG TCC CTG GAG AGC 3' (SEQ. ID. No. ~~1~~ 4), which is a forward primer, and

(b) 5' TGC CTC GTC CGC ATT CAC CCT TCA GAC TGC 3' (SEQ. ID. No. ~~2~~ 3). which is a reverse primer.

Claim 3 (Original): A method as claimed in claim 1 wherein the length of oligonucleotide primers of said oliognucleotide primers is between 5 and 100 bases.

Claim 4 (Original): A method as claimed in claim 1 wherein, the SP-A2 gene has allelic variants which have G/C and A/G halotypes.

Claim 5 (Withdrawn): A diagnostic kit for the detection of single nucleotide polymorphisms (G/C at 1649 position and A/G at 1660 position) comprising primers selected from the group consisting of: (a) 5' TGC CTG GAG CCC CTG GTG TCC CTG GAG AGC 3' (SEQ. ID. No. 1), which is a forward primer, and (b) 5' TGC CTC GTC CGC ATT CAC CCT TCA GAC TGC 3' (SEQ. ID. No. 2), which is a reverse primer.

Claim 6 (Withdrawn): Primers suitable for amplification of SP-A2 gene region containing one or more polymorphic sites, said primer selected from the group consisting of: (a) 5' TGC CTG GAG CCC CTG GTG TCC CTG GAG AGC 3' (SEQ. ID. No. 1), which is a forward primer, and (b) 5' TGC CTC GTC CGC ATT CAC CCT TCA GAC TGC 3' (SEQ. ID. No. 2), which is a reverse primer.